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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/089,501

DATE: 11/07/2002
 TIME: 15:18:12

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3 <110> APPLICANT: SAITO, HIROYUKI
 4 KITAZAWA, TAKEHISA
 5 YOSHIHASHI, KAZUTAKA
 6 HATTORI, KUNIHIRO
 8 <120> TITLE OF INVENTION: PREVENTION AND TREATMENT OF BLOOD COAGULATION-RELATED
 9 DISEASES
 11 <130> FILE REFERENCE: 053466-0325
 13 <140> CURRENT APPLICATION NUMBER: 10/089,501
 14 <141> CURRENT FILING DATE: 2002-03-29
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP00/06802
 17 <151> PRIOR FILING DATE: 2000-09-29
 19 <150> PRIOR APPLICATION NUMBER: JP 11-281843
 20 <151> PRIOR FILING DATE: 1999-10-01
 22 <150> PRIOR APPLICATION NUMBER: JP 11-282120
 23 <151> PRIOR FILING DATE: 1999-10-01
 25 <150> PRIOR APPLICATION NUMBER: JP 11-282134
 26 <151> PRIOR FILING DATE: 1999-10-01
 28 <150> PRIOR APPLICATION NUMBER: JP 11-282167
 29 <151> PRIOR FILING DATE: 1999-10-01
 31 <150> PRIOR APPLICATION NUMBER: JP 11-282188
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 34 <150> PRIOR APPLICATION NUMBER: JP 11-282192
 35 <151> PRIOR FILING DATE: 1999-10-01
 37 <160> NUMBER OF SEQ ID NOS: 104
 39 <170> SOFTWARE: PatentIn Ver. 2.1
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 43 <212> TYPE: DNA
 44 <213> ORGANISM: Artificial Sequence
 46 <220> FEATURE:
 47 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 48 MHC-G1
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 60 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 61 MKC
 63 <400> SEQUENCE: 2 27
 64 ggatcccggg tggatggtgg gaagatg

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73 <223> OTHER INFORMATION: Description of Artificial Sequence: M13 Primer
74     M4 sequence
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77 gttttcccag tcacgac
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82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
85 <220> FEATURE:
86 <223> OTHER INFORMATION: Description of Artificial Sequence: M13 Primer
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89 <400> SEQUENCE: 4                                17
90 caggaaacag ctatgac
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94 <211> LENGTH: 408
95 <212> TYPE: DNA
96 <213> ORGANISM: Mus sp.
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (1)..(408)
102 <220> FEATURE:
103 <221> NAME/KEY: sig_peptide
104 <222> LOCATION: (1)..(57)
106 <220> FEATURE:
107 <221> NAME/KEY: mat_peptide
108 <222> LOCATION: (58)..(408)
109 <223> OTHER INFORMATION: Nucleotide sequence coding for H chain V region of
110     anti-TF mouse monoclonal antibody ATR-5
112 <400> SEQUENCE: 5
113 atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg      48
114 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly
115     -15     -10     -5
117 gtc aat tca gag gtt cag ctg cag cag tct ggg act aac ctt gtg agg      96
118 Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Thr Asn Leu Val Arg
119     -1     1     5     10
121 cca ggg gcc tta gtc aag ttg tcc tgc aaa ggt tct ggc ttc aac att      144
122 Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Gly Ser Gly Phe Asn Ile
123     15     20     25
125 aaa gac tac tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg      192
126 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu
127     30     35     40     45
129 gag tgg att gga ggg aat gat cct gcg aat ggt cat agt atg tat gac      240
130 Glu Trp Ile Gly Gly Asn Asp Pro Ala Asn Gly His Ser Met Tyr Asp
131     50     55     60

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133 ccg aaa ttc cag ggc aag gcc agt ata aca gca gac aca tcc tcc aac 288
134 Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn
135          65          70          75
137 aca gcc tac ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc 336
138 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
139          80          85          90
141 tat ttc tgt gct aga gac tcg ggc tat gct atg gac tac tgg ggt caa 384
142 Tyr Phe Cys Ala Arg Asp Ser Gly Tyr Ala Met Asp Tyr Trp Gly Gln
143          95          100          105
145 gga acc tca gtc acc gtc tcc tca 408
146 Gly Thr Ser Val Thr Val Ser Ser
147 110          115
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151 <211> LENGTH: 381
152 <212> TYPE: DNA
153 <213> ORGANISM: Mus sp.
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (1)..(381)
159 <220> FEATURE:
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163 <220> FEATURE:
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165 <222> LOCATION: (61)..(381)
166 <223> OTHER INFORMATION: Nucleotide sequence coding for L chain V region of
167 anti-TF mouse monoclonal antibody ATR-5
169 <400> SEQUENCE: 6
170 atg agg gcc cct gct cag ttt ttt ggg atc ttg ttg ctc tgg ttt cca 48
171 Met Arg Ala Pro Ala Gln Phe Phe Gly Ile Leu Leu Leu Trp Phe Pro
172 -20          -15          -10          -5
174 ggt atc aga tgt gac atc aag atg acc cag tct cca tcc tct atg tat 96
175 Gly Ile Arg Cys Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr
176          -1 1          5          10
178 gca tcg ctg gga gag aga gtc act atc act tgc aag gcg agt cag gac 144
179 Ala Ser Leu Gly Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp
180          15          20          25
182 att aaa agc ttt tta agt tgg tac cag caa aaa cca tgg aaa tct cct 192
183 Ile Lys Ser Phe Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro
184          30          35          40
186 aag acc ctg atc tat tat gca aca agc ttg gca gat ggg gtc cca tca 240
187 Lys Thr Leu Ile Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser
188          45          50          55          60
190 aga ttc agt ggc agt gga tct ggg caa gat tat tct cta acc atc aac 288
191 Arg Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Asn
192          65          70          75
194 aac ctg gag tct gac gat aca gca act tat tat tgt cta cag cat ggt 336
195 Asn Leu Glu Ser Asp Asp Thr Ala Thr Tyr Tyr Cys Leu Gln His Gly
196          80          85          90

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198 gag agc ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa      381
199 Glu Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
200          95          100          105
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204 <211> LENGTH: 35
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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212 <400> SEQUENCE: 7      35
213 gtctgtcgac ccaccatgaa atgcagctgg gtcat
216 <210> SEQ ID NO: 8
217 <211> LENGTH: 28
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221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
223      ch5HA
225 <400> SEQUENCE: 8      28
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229 <210> SEQ ID NO: 9
230 <211> LENGTH: 35
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
236      ch5LS
238 <400> SEQUENCE: 9      35
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244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
249      ch5LA
251 <400> SEQUENCE: 10      28
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256 <211> LENGTH: 104
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260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence: CDR grafting
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264 <400> SEQUENCE: 11
265 ttctgtcgac ccaccatgaa atgcagctgg gtcatttct tcctgatggc agtggttaca 60
266 ggggttaact cacaggtgca gctgttgagg tctggagctg tgct      104

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275 <223> OTHER INFORMATION: Description of Artificial Sequence: CDR grafting
276     primer hr5Hv2S
278 <400> SEQUENCE: 12
279 acaggtgcag ctgttgagctgt gctggcaagg cctgggactt cctgaagat 60
280 ctccctgaag gcttccggtat tcaacattaa agactactat atgcattg 108
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285 <212> TYPE: DNA
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289 <223> OTHER INFORMATION: Description of Artificial Sequence: CDR grafting
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292 <400> SEQUENCE: 13
293 gaatggccat agtatgtatg acccgaaatt ccagggcagg gccaaactga ctgcagccac 60
294 atccgccagt attgcctact tggagttctc gagcctgaca aatgagga 108
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299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence: CDR grafting
304     primer hr5Hv3A
306 <400> SEQUENCE: 14
307 tcatacatatc tatggccatt cgcaggatca ttcccaccaa tccattctag accctgtcca 60
308 ggcctctgtt ttacccaatg catatagtag tctttaatgt tgaatccgga 110
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318     primer hr5Hv5A
320 <400> SEQUENCE: 15
321 agaagctagc tgaggagacg gtgaccaggg tgccttggcc ccagtagtcc atggcatagc 60
322 ccgagtctct tgcacagtaa tagaccgcag aatcctcatt tgtcaggctc 110
325 <210> SEQ ID NO: 16
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327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
332     hr5HvPrS
334 <400> SEQUENCE: 16
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